

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 13:04:36 ; Search time 5356.8 seconds  
(without alignments)  
17812.975 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169  
Sequence: 1 aatcttgctcagttactctc.....cttggtccctccatgtcag 6169

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 8

Total number of hits satisfying chosen parameters: 2551636

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_om:\*  
43: em\_or:\*

44: em\_ov:\*  
45: em\_pat:\*  
46: em\_ph:\*  
47: em\_pl:\*  
48: em\_ro:\*  
49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_v1:\*  
53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
58: gb\_v11:\*  
59: gb\_v12:\*  
60: gb\_htg1:\*  
61: gb\_htg2:\*  
62: gb\_htg3:\*  
63: gb\_htg4:\*  
64: gb\_htg5:\*  
65: gb\_htg6:\*  
66: gb\_htg7:\*  
67: gb\_htg8:\*  
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84: gb\_htg25:\*  
85: gb\_pr1:\*  
86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_r01:\*  
95: gb\_r02:\*  
96: gb\_in4:\*  
97: gb\_pr10:\*  
98: em\_ba3:\*

pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5552	90.0	79376	92 HS454G6	298750 Human DNA s
2	5300	85.9	5300	88 AF007562	AF007562 Homo sapi
3	5243	85.0	170425	68 AC024490	AC024490 Homo sapi
4	2285	37.0	2800	93 HSMYOC1	AF049791 Homo sapi
5	1035	16.8	1086	93 HSGIC1A1	Z57171 Homo sapien
6	978	15.9	1228	85 AB006686S1	AB006686 Homo sapi
7	647	10.5	1934	91 D88214	D88214 Homo sapien
8	640	10.4	1871	9 AX004457	AX004457 Sequence

9	640	10.4	1871	9	AX004474	AX004474	Sequence
10	640	10.4	1939	9	AR030962	AR030962	Sequence
11	640	10.4	1939	9	AR066022	AR066022	Sequence
12	640	10.4	1939	9	AR069089	AR069089	Sequence
13	640	10.4	2000	97	HSU85257	U85257	Human trabe
14	640	10.4	2002	9	AB4847	AB4847	Sequence 2
15	625	10.1	2051	93	HSAF001620	AF001620	Homo sapi
16	604	9.8	1512	9	AB4848	AB4848	Sequence 3
17	604	9.8	1512	9	AR030963	AR030963	Sequence
18	604	9.8	1512	9	AR066023	AR066023	Sequence
19	604	9.8	1512	9	AR069090	AR069090	Sequence
20	594	9.6	2000	9	AB4850	AB4850	Sequence 2
21	558	9.0	1512	9	AB4851	AB4851	Sequence 3
22	366	5.9	1969	9	AR020502	AR020502	Sequence
23	366	5.9	1969	10	I36470	I36470	Sequence 2
24	330	5.3	1491	9	AR020503	AR020503	Sequence
25	330	5.3	1491	10	I36471	I36471	Sequence 3
26	189	3.1	228	88	AF007564	AF007564	Homo sapi
27	74	1.2	49868	78	AC090368	AC090368	Homo sapi
28	74	1.2	73431	82	AP000575	AP000575	Homo sapi
29	74	1.2	109290	84	HS838L14	Y12335	Homo sapien
30	74	1.2	157454	82	AP001462	AP001462	Homo sapi
31	74	1.2	166269	82	AP001187	AP001187	Homo sapi
32	74	1.2	171980	82	AP000928	AP000928	Homo sapi
33	74	1.2	176653	82	AP001857	AP001857	Homo sapi
34	74	1.2	178100	82	AP001558	AP001558	Homo sapi
35	74	1.2	203300	85	AC000134	AC000134	Homo sapi
36	72	1.1	200422	73	AC068553	AC068553	Homo sapi
37	70	1.1	153831	75	AC079168	AC079168	Homo sapi
38	70	1.1	199937	86	AC007055	AC007055	Homo sapi
39	65	1.1	111107	86	AC005924	AC005924	Homo sapi
40	65	1.1	164945	68	AC024251	AC024251	Homo sapi
41	65	1.1	175336	83	CNS01D7Q	AL132838	Homo sapi
42	64	1.0	136886	89	AL138889	AL138889	Human DNA
43	64	1.0	168210	87	AC018719	AC018719	Homo sapi
44	64	1.0	168544	89	AL133344	AL133344	Human DNA
45	64	1.0	179040	67	AC022732	AC022732	Homo sapi

## ALIGNMENTS

RESULT 1	HS454G6/c	79376 bp	DNA	PRI	23-NOV-1999
LOCUS	Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains				
DEFINITION	trabecular meshwork inducible glucocorticoid response protein,				
	TIGR, myocillin, ESTs and STS.				
ACCESSION	Z98750				
VERSION	Z98750.1	GI:2887277			
KEYWORDS	1q24; myocillin; TIGR.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 79376)				
AUTHORS	Deadman,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-OCT-1997) Chromosome 1 Project Group				
	(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,				
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:				
	humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk				
	On Feb 14, 1998 this sequence version replaced gi:2465060.				
	IMPORTANT: This sequence is not the entire insert of clone 454G6.				
	It may be shorter because we only sequence overlapping sections				
	once, or longer because we arrange for a small overlap between				
	neighbouring submissions.				
	During sequence assembly data is compared from overlapping clones.				
	Where differences are found these are annotated as variations				
	together with a note of the overlapping clone name. Note that the				
	variations annotated may not be found in the sequence submission				
	corresponding to the overlapping clone as we submit sequences with				
	only a small overlap as described above.				

## FEATURES

source	This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr1/">http://www.sanger.ac.uk/HGP/Chr1/</a>
	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
	The true left end of clone 454G6 is at 1 in this sequence. The true left end of clone 560B9 is at 79273.
	454G6 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
	For further details see <a href="http://bacpac.med.buffalo.edu/">http://bacpac.med.buffalo.edu/</a> .
	Location/Qualifiers
	1..79376
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="1"
	/map="1q24"
	/clone="RP3-454G6"
	/clone.lib="RPC1-3"
repeat_region	435..472
	/note="19 copies of 2 mer 82 & conserved"
prim_transcript	1914..>3968
	/note="match: multiple ESTs
	match: R56676 AA043968 W63639 F12081 AA046699
	match: F02925 AA131540 R36066 AA131383
	match: AA163561 F02925 AA131540 W00634 R36066
	match: AA131383 AA163561 N89173 AA174814 AA057059
	match: AA329084 W47082 AA043955 AA341783 AA353681
	match: AA046487 AA369741 H08313 AA186895 H32730
	match: H08333 H08236 N42052 D61944 R27102 N32353
	match: N30491 AA307150 AA192"
repeat_region	3703..3746
	/note="22 copies of 2 mer 89 & conserved"
repeat_region	4051..4183
	/note="AluSq repeat: matches 1..133 of consensus
	incomplete repeat"
repeat_region	4200..4502
	/note="AluSq repeat: matches 2..301 of consensus"
	4659..4851
	/note="AluSx repeat: matches 2..194 of consensus
	incomplete repeat"
repeat_region	5216..5345
	/note="AluDo repeat: matches 132..1 of consensus
	incomplete repeat"
repeat_region	7759..7907
	/note="MIR repeat: matches 174..1 of consensus"
repeat_region	7933..9328
	/note="TIGER1 repeat: matches 1..1472 of consensus"
repeat_region	9332..9626
	/note="AluSg repeat: matches 1..289 of consensus"
repeat_region	9639..10335
	/note="TIGER1 repeat: matches 1469..2174 of consensus"
repeat_region	10343..10642
	/note="AluSg repeat: matches 1..300 of consensus"
repeat_region	10643..10856
	/note="TIGER1 repeat: matches 2175..2417 of consensus"
	<10903..>16855
	/note="endogenous retroviral sequence"
misc_feature	10949..11384
repeat_region	/note="LTR2 repeat: matches 31..449 of consensus"
repeat_region	15835..15870
	/note="18 copies of 2 mer 83 & conserved"
repeat_region	16856..17286
	/note="LTR2 repeat: matches 31..449 of consensus"
repeat_region	17287..17574
	/note="AluSg repeat: matches 15..300 of consensus"
repeat_region	18294..18650
	/note="THE1B repeat: matches 358..1 of consensus"
repeat_region	18877..19180

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/note="Aluy repeat: matches 301. .2 of consensus"
19767. .20013
/note="MLR2_internal repeat: matches 5002. .4750 of
consensus"
repeat_region
20051. .20118
/note="MLR1F repeat: matches 539. .471 of consensus"
20130. .20261
/note="Aluub repeat: matches 131. .1 of consensus
incomplete repeat"
20264. .20722
/note="MLR1F repeat: matches 482. .1 of consensus"
20858. .21223
/note="MSYD repeat: matches 394. .1 of consensus"
21216. .21302
/note="MLR2_internal repeat: matches 4520. .4433 of
consensus"
21403. .21703
/note="MLR2_internal repeat: matches 3887. .3580 of
consensus"
21978. .22357
/note="MLR2_internal repeat: matches 3218. .2839 of
consensus"
22363. .22524
/note="MLR2_internal repeat: matches 2495. .2317 of
consensus"
22531. .22839
/note="AlusX repeat: matches 302. .1 of consensus"
23007. .23309
/note="AlusP repeat: matches 3. .301 of consensus"
23286. .>23680
/note="STS G07544"
complement(23652. .24072)
/note="STS G07436"
24008. .24290
/note="AluJo repeat: matches 298. .6 of consensus"
25895. .26364
/note="LTR2 repeat: matches 2. .449 of consensus"
26397. .26697
/note="AlusG repeat: matches 1. .302 of consensus"
26719. .27021
/note="AlusX repeat: matches 1. .302 of consensus"
29037. .29334
/note="AlusX repeat: matches 300. .3 of consensus"
30028. .30310
/note="AlusX repeat: matches 1. .301 of consensus"
30402. .30539
/note="MLR2B repeat: matches 264. .404 of consensus"
30402. .30615
/note="MLR2A repeat: matches 264. .453 of consensus"
<30801. .>31136
/note="match: 5' EST AA256902 clone 682136"
30980. .31222
/note="MER4B repeat: matches 199. .431 of consensus"
31232. .31528
/note="AlusG repeat: matches 299. .1 of consensus"
31530. .31654
/note="MER4B repeat: matches 417. .540 of consensus"
31836. .32135
/note="Aluy repeat: matches 300. .1 of consensus"
32200. .32301
/note="AluJo repeat: matches 186. .287 of consensus
incomplete repeat"
32365. .32493
/note="MIR repeat: matches 206. .67 of consensus"
33283. .33399
/note="MIR repeat: matches 77. .196 of consensus"
33408. .33667
/note="Aluy repeat: matches 1. .291 of consensus"
33956. .34043
/note="MIR repeat: matches 80. .167 of consensus"
34725. .34904
/note="AluJo repeat: matches 299. .127 of consensus
incomplete repeat"
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repeat_region 34907. .35207
/note="Aluy repeat: matches 300. .1 of consensus"
35212. .35344
repeat_region
/note="Aluub repeat: matches 133. .1 of consensus
incomplete repeat"
36545. .36842
repeat_region
/note="AluJo repeat: matches 299. .1 of consensus"
38190. .38379
/note="MER3 repeat: matches 209. .13 of consensus"
38382. .38682
repeat_region
/note="AlusX repeat: matches 1. .302 of consensus"
38836. .38968
repeat_region
/note="MIR2 repeat: matches 145. .2 of consensus"
38983. .39279
repeat_region
/note="AluJo repeat: matches 3. .296 of consensus"
39418. .39773
/note="THE1A repeat: matches 354. .2 of consensus"
39775. .40120
/note="THE1B-INTERNAL repeat: matches 1580. .1234 of
consensus"
repeat_region 40757. .41023
/note="AluJo repeat: matches 37. .301 of consensus
incomplete repeat"
41307. .41589
repeat_region
/note="Alusq repeat: matches 21. .303 of consensus

Query Match 90.0%; Score 5552; DB 92; Length 79376;
Best Local Similarly 99.9%; Pred. No. 0;
Matches 6022; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

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Db 68406 ATCTTTGTTCAATTACTCTCAGGCGTATTATGAATGAATGAATACCATGTGAAG 68347

Qy 61 tccataaactgataagcctccatcgcgatgatagtctcttgccagagatgaataatca 120
Db 68346 TCCATATAACGTATPAGCGCTCATTTCCGATGTATGTCTTGGCAGAGATGAAGATCA 68287

Qy 121 ggaagaagagatccacglttagccaagtgccagcgtgctgctcttaattgta 180
Db 68286 GGAAGAAAGAGACTATCCAGTTAGCCAAAGTGTCCAGCGCTGTCTGTATTTAGTGA 68227

Qy 181 cagatgtgctccctgaagagactatcttcaaggaatacatatccaatgtgtaattc 240
Db 68226 CAGATGTTGCTCTGACGGAAGCTATTCTTCAGGAATATCATCCAAATGGTAATTC 68167

Qy 241 catcaaacagagatgaagaacaggaatgagatgagcactgcccagaagaaatgcag 300
Db 68166 CATCAACAGAGAGATGAAGAAACAGGAATGAGATGGCGCTGCCCAAGAAATGCGCAG 68107

Qy 301 gaggcaataatgatagaataataacttcccttgctttaaattcaggaaaaatg 360
Db 68106 GAGAGCAAAATATGATGAATAATTAACCTTTCCCTTTGTTTAAATTCACAGAAATAATG 68047

Qy 361 atggagaccataatcaatgaataaggaacagctcgaagaaagaatgattccaatgg 420
Db 68046 ATGAGGACCAAAATCAATGAATTAAGAAACAGCTCACAAAAAAGATCTTCCAAATTTGG 67987

Qy 421 taatlaagtatttctcttggaagagacctcactgtaagcttgatgagaaatggaa 480
Db 67986 TAAATTAAGTATTGTGCTCTTGGAAAGACCTCCATGTGACTTGTATGGAAATGGAA 67927

Qy 481 aaacgtcaaaagcatgcatcagatcccaagaatgatatatttaaaaccagat 540
Db 67926 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGATTAATTTTAAAAACCGAT 67867

Qy 541 ggcactcctggggaggaagctcaggaaggtcatgtttagcaagaagcataaacaatac 600
Db 67866 GGCAATCACTCTGGGGAGGCAAGTTCAAGAAAGTCAATGTATTACCAAGGACATTAAC 67807

Qy 601 agcaaaatcaaatccgcaaatcaggaaggaataatggggcttggaagcttcataac 660
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OY 661 agtgaatagcagltgacacatgttcgacaacccctccgctctataccagggaacacaaa 720  
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Db 67626 GACATGGTTAAAAGGACACAGAACATGTGAGCCTTCAAGACAGCTCCCTCAGCA 67567  
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OY 901 tgaagaagacatgaatttcaacatttcaagtaaaacaataatgcataatcaag 960  
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Db 67446 TTTAGACATGGGTCCCATTTTATAAGTCAGGCATACAGATACGTGTCCAGCTCC 67387  
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OY 1681 caatggctcactcaacttcttccctcaactcacttcaaggtcaaggttaacattcaat 1740  
|||||  
Db 66726 CACTGTCTCATCACTTTCTTCTCCCTCATCCCTCATTTTTCAGGCTAAGTTAACCTTTATTT 66667

OY 1741 cacatgcttctgtggaagcctccacatcgttactgaaataagagtatatacaactag 1800  
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Db 66666 CACCATGCTTTTGTGTAACCTCCACATGTTACTGAATTAAGAGATATCATTAACCTAG 66607  
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Db 66606 TTCCATTTGGGGCATCTGTGTGTATAGGGGAGGAGGAGATACCCAGAGACTCTT 66547  
OY 1861 tgaagcccccagagaggttctctcccaacttgagggaagccctgcagaaccccgggtcc 1920  
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Db 66546 TGAAGCCCCGGGAGAGGTTCTCTCCACACTGGGGAGGCCCTGCAGACGCCGGGTCC 66487  
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Db 66426 GACCTGTGCTTCTATTTCTGTGTGATGACCTGTTCAATTCACAGCATTTGACAAAT 66367  
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			18-MAR-1998

DEFINITION	Homo sapiens trabecular meshwork inducible glucocorticoid response protein (TIGR) gene, promoter region and partial mRNA sequence.
ACCESSION	AF007562
VERSION	AF007562.1
KEYWORDS	GI:2970123
SOURCE	.
ORGANISM	human. Homo sapiens
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TITLE	JOURNAL MEDLINE U. Biol. Chem. 273 (11), 6341-6350 (1998) 98165818
REFERENCE	2 (bases 1 to 5300) Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R. Direct Submission Submitted (10-JUN-1997) Ophthalmology, University of California San Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA
AUTHORS	Polansky,J.R.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 5863; Conservative 0; Mismatches 4; Indels 4; Gaps 3;
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Db	69363	CAGAGAGGGCTGCAAGAGGAGACTGGGCACCTTGAGCGCGAGAGCGGACNACTTGAAAC	69422
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Oy	5796	gagagagaagaagcgactaagcacaagaataatgaaatctgtgcgcagaagaggttggaaaaagc	5855
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AUTHORS	Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Atbour,N.C.,		
	Alward,W.L.W., Sheffield,V.C. and Stone,E.M.		
TITLE	Characterization and comparison of the human and mouse GLCIA		
JOURNAL	glaucoma genes		
REFERENCE	Genome Res. (1998) In press		
AUTHORS	2 (bases 1 to 2800)		
	Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Atbour,N.C.,		
	Alward,W.L.W., Sheffield,V.C. and Stone,E.M.		
	Direct Submission		
TITLE	Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200		
JOURNAL	Hawkins Drive, Iowa City, IA 52242, USA		

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 REFERENCE 1 (bases 1 to 1086)  
 Stone, E.M., Pingert, J.H., Alward, W.L., Nguyen, T.D., Polansky, J.R., Sundén, S.L., Nishimura, D., Clark, A.F., Nystuen, A., Nichols, B.E., Ritch, R., Kalenak, J.W., Craven, E.R. and Shefffield, V.C.  
 Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997)  
 TITLE JOURNAL MEDLINE 97158493  
 REFERENCE 2 (bases 1 to 1086)  
 Adam, M.F., Belmonte, A., Binisti, P., Brezin, A.P., Valtot, F., Becheville, A., Dascotte, J.C., Copin, B., Gomez, L., Chaventre, A., Bach, J.F. and Garçon, H.J.  
 Recurrent mutations in a single exon encoding the evolutionarily conserved olfactomedin-homology domain of TRK in familial open-angle glaucoma Hum. Mol. Genet. 6 (12), 2091-2097 (1997)  
 JOURNAL





JOURNAL MEDLINE REFERENCE AUTHORS	J. Blochchem. 118 (5), 921-931 (1995) 96318503
JOURNAL MEDLINE REFERENCE AUTHORS	2 (sites) Stone, E.M., Flinger, J.H., Alward, W.L., Nguyen, T.D., Polansky, J.R., Sunden, S.L., Nishimura, D., Clark, A.F., Nyström, A., Nichols, B.E., Ritch, R., Kalenak, J.W., Craven, E.R. and Sheffield, V.C. Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997) 97158493
JOURNAL MEDLINE REFERENCE AUTHORS	3 (sites) Kubota, R., Noda, S., Wang, Y., Minoshima, S., Asakawa, S., Kudoh, J., Mashima, Y., Oguchi, Y. and Shimizu, N. A novel myosin-like protein (myoclin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping Genomics 41 (3), 360-369 (1997) 97312692
JOURNAL MEDLINE REFERENCE AUTHORS	4 (sites) Kubota, R., Kudoh, J., Mashima, Y., Asakawa, S., Minoshima, S., Hejranic, J.F., Oguchi, Y. and Shimizu, N. Genomic Organization of the human myoclin gene (MYOC) responsible for primary open angle glaucoma (GIC1a) Biochem. Biophys. Res. Commun. 242 (2), 396-400 (1998) 98113364
JOURNAL MEDLINE REFERENCE AUTHORS	5 (bases 1 to 1228) Shimizu, N. and Kudoh, J. Direct Submissio Submitted (16-AUG-1997) to the DDBJ/EMBL/Genbank databases.

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AUTHORS	1 (bases 1 to 1934)			
TITLE	Shimizu, N.			
JOURNAL	Direct Submission			
	Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.			

MoBuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@med.keio.ac.jp, Tel:03-3351-2370, Fax:03-3351-2370)

2 (sites)

REFERENCE  
AUTHORS  
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REFERENCE 1 (bases 1 to 1871)  
AUTHORS Anctil,J.L. and Cote,G.  
TITLE Molecular diagnosis of glaucomas associated with chromosomes 1,  
and method of treatment thereof  
JOURNAL Patent: WO 9916898-A 1 08-APR-1999;  
ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)  
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Db 301	AAAGCTCGACTCAGCTCCCTGGAGACCTCTCTCCACCAATTGACCTTGACACAGCTGCTCC	360												
Oy 5661	aggccccaagagaccccaagagagctctgacagagagactgagacaccttgagagcagagag	5720												
Db 361	AGGCCCCAGAGACCCAGAGAGGGCGCTGCGAGAGGAGACTTGGCACTTGAGCCGGAGACCG	420												
Oy 5721	gaccagcttgaaacccaacacagagaggttgtagagctctgctacagcaacctctccagagac	5780												
Db 421	GACAGAGCTTGAAACCCAAACCCAGAGAGTGTGGAGAGACTGCTACAGCAACCTCTCCGAGAC	480												
Oy 5781	aagctagctcttgagagagagagagagagagacacaaagagaaatagagaaatctgagccag	5840												
Db 481	AAGTCAGTTCTTGAGAGAGAGAGAGAGAGGACCTTAAGGCAAGAAATGAGATCTGGCCAGG	540												
Oy 5841	aggcttgaaagcagcagcagcagagaggttagcagaagctctgagagagggcgcaagtctccacag	5900												
Db 541	AGGTTGGAAGACGACGACGACGAGGAGGAGCAAGAGCTGAGAGAGGGCGCAGTGTCCCGAGAC	600												
Oy 5901	cgagagacactgctccgggctctgcccacacagagctccagagaag	5940												
Db 601	CGAGACACTGCTCGGGGCTGTGCCACACAGGCTCCAGAGAG	640												
RESULT 9														
AX004474	AX004474	1871 bp	DNA	PAT	24-AUG-2000									
LOCUS	Sequence 18 from Patent W0916898.													
DEFINITION	AX004474													
ACCESSION	AX004474.1	GI:9927933												
VERSION														
KEYWORDS														
SOURCE	human.													
ORGANISM	Homo sapiens													
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.													
REFERENCE	1 (bases 1 to 1871)													
AUTHORS	Anttil,J.L. and Cote,G.													
TITLE	Molecular diagnosis of glaucomas associated with chromosomes 1,													
	and method of treatment thereof													
	Patent: WO 9916898-A 18 08-Apr-1999;													
	ANCTIL JEAN LOUIS (CA); COTE GILES (CA)													
JOURNAL	Location/Qualifiers													
FEATURES	1..1871													
source	/organism="Homo sapiens"													
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	GROYTTSVASPNSSCEPEOSQAMSVLHNLRDSSSTGRDLDEATRKARLSLESLIHQDL													
	TLDDAARPEOTEGLORELGTLRRERQULETQRELEBTAYSNLRDSELEEKRLR													
	QENLNARPLESSQSEVARRLRGCGPOTRDAFVPPGSRFSTWNLNDTLAFOJLASEE													
	LTEVPASRLIKESPGVGLRSGEDGTGGELWVGEPLRLTAEITITKYGWMDPKPR													
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	Query Match	10.4%	Score 640;	DB 9;	Length 1871;
	Best Local Similarity	100.0%:	Pred. No. 0;		
	Matches 640; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
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Dd	1 AGAGCTTTCACAGAAGACTCACCAGGCGTTGCATGAGGTCTTGTCGACACTGC	60			

QY	5361	tgaaagctttggagccttgagatgagcaagctgttccaaagtctgcttcttgccgtcctggttggtg	5420
Db	61	ttccacctttttgggacctggaatgtccagctgtccacctctctcttcttgccctgctgtgtgg	120
QY	5421	ga tgc tggggggcccaagaacagctccaagtccaagaaagccaatggaccagatgtgcctga tggcag	5480
Db	121	gattgtggggggcccaagacagctccaagcttagaagaagcccaattgaccagagtggccgattggcag	180
QY	5481	tataacctcaag tgtgtgcgaag tcccaatgaa tcccaagctgtgcccaagacaagaacgaagcca tgc	5540
Db	181	tattacctttcaagttgtggccagaccatcccaatgaattccagctgtgcccaagacagaccagaccatgc	240
QY	5541	tcaagtcacatcaataacttaacagagaagaagaagacccaagcgtttagaccttggaagccacc	5600
Db	241	ttcagtcattccatattactttacgaagagacagacagaccacaaacgctttagaccttggaagccacc	300
QY	5601	aaagctctgaacccaagctccctctggaagagcctctccaccaa ttgaaccttgaaccaagctatcc	5660
Db	301	aaagcttcgaacccaagctccctctggaagagcctctccaccaa ttgaaccttgaaccaagctatcc	360
QY	5661	aggcccacgaagaccccaagagaggtctgcagaaggaagcttggcacccttgaaagcgtggaagctgcg	5720
Db	361	aggcccacgaagaccccaagagagaggtctgcagaaggaagcttggcacccttgaaagcgtggaagctgcg	420
QY	5721	gaacagctcggaataaccbaaaccaagaagatttggaagactgccttaagaacaactctctccgagac	5780
Db	421	gaacagctcggaataaccbaaaccaagaagatttggaagactgccttaagaacaactctctccgagac	480
QY	5781	aagtcagttctgcggaggaagaagaagcgaactgaagccaagaatctgaaatctctgtgccag	5840
Db	481	aagtcagttctgcggaggaagaagaagcgaactgaagccaagaatctgaaatctctgtgccag	540
QY	5841	aggttggaagaacgaacgaacccaaggaatgaacaagctctgaaagaagggccag tgtccccaagcc	5900
Db	541	aggttggaagaagaacgaacccaaggaatgaacaaggaagggccag tgtccccaagcc	600
QY	5901	cgagaaactgtctgggtctgtgcaccaacgaagctccaagaagaag	5940
Db	601	cgagaaactgtctgggtctgtgcaccaacgaagctccaagaagaag	640

LOCUS	AR030962	1999 bp	DNA	PAT	29-SEP-1999
DEFINITION	Sequence 2 from patent US 5861497.				
ACCESSION	AR030962				
VERSION	AR030962.1 GI:5944176				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1999)				
AUTHORS	Nguyen,T.D., Polansky,J.R. and Huang,W.				
TITLE	Tribecular meshwork induced glucocorticoid response (TIGR) nucleic acid molecules				
JOURNAL	Patent: US 5861497-A 2 19-JAN-1999;				
FEATURES	Location/Qualifiers				
source	1..1999				
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BASE COUNT	537 a	508 c	534 g	420 t	
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Best Local Similarity	100.0%; Pred. No. 0;				
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Db 1	AGAGCTTTCACAGAGAAAGCCTCACCAAGCCTTGCAATGAGGTTCTCTGTGCACGTTGC 60				
Y 5361	tgcaccttcggcccgagatgcacagctgtccagctgtgctctgtgacctgactgtgttg 5420				

Dd	61	ttccaccttttggggcccttcgaatatcccaactgtccacagctgcgtcttcttgccctccctccgtgtggc	120			
Oy	5421	gatgtg99ggcccaagacagcgtcaccgtccagaagcccaatgaccagagtgtgcccgaatgccaag	5480			
Dd	121	gatgtg9ggggccagacagctacgtctcaggaagggccaatgacacagatggtggccgatgccag	180			
Oy	5481	ctatgccttcagtgtgtgcccaggtcccaatgaatctccagctgtgccaaagacaaagccagccatg	5540			
Dd	181	tatatcctttcagtggtggccagctcccaatgaatccacactctccacagacacagccagccagtgtg	240			
Oy	5541	tcagatccatcaatcaatctacaagagacagcaagcaaccagcctctagacctgtgaagccacc	5600			
Dd	241	ttcagctatctccatcaattttacagagacacagacacaccacactttagaccttgagaccacacc	300			
Oy	5601	aaagctctgactcagctccctgtgaagagcctctcccaatctgacctgtgaccagagctgtcc	5660			
Dd	301	aaagcttcgactcagctccctgtgaagagcctctcccaatctgacctgtgaccagagctgtcc	360			
Oy	5661	aggcccccagagagaccacaaagagggagctgtcagaagggagagctctgggacaccctgaagccggaagcgg	5720			
Dd	361	aggcccccagagagaccacaaagagggagctgtcagaagggagagctctgggacaccctgaagccggaagcgg	420			
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Dd	421	gaccagcctgtgaagaccacaaagagagatgttgagagctgtcctacagcaactccctccgagac	480			
Oy	5781	aagtcagctctctgtgaagagagagagagagctaaagggacagaaatgagaaatctgtgccaag	5840			
Dd	481	aagtcagctctctgtgaagagagagagagagagctaaagggacagaaatgagaaatctgtgccaag	540			
Oy	5841	aggtctgtgaagagacagacagccagagaggtagcaaggtctgagaaggggagctgtgtcccaagc	5900			
Dd	541	aggtctgtgaagagacagacagccagagaggtagcaaggtctgagaaggggagctgtgtcccaagc	600			
Oy	5901	cgaagacactgtcctggagctgtgtgcccacacaggtctcacaagag	5940			
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DEFINITION	Sequence 2 from patent US 5849879.					
ACCESSION	AR06022					
VERSION	AR06022.1 GI:5996238					
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1999)					
AUTHORS	Nguyen,T.D., Polansky,J.R. and Huang,W.					
TITLE	Methods for the diagnosis of glaucoma.					
JOURNAL	Patent: US 5849879-A 2 15-DEC-1998;					
FEATURES	Location/Qualifiers					
source	1..1999					
BASE COUNT	537 a 508 c 534 g 420 t					
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Query Match 10.4%; Score 640; DB 9; Length 1999;						
Best Local Similarity 100.0%; Pred. No. 0;						
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Dd	1	AGAGCTTTCCACAGAGAACGCTCACCAAGCGCTTCGAATGAGGTTTCTGTGCACAGTTGC	60			
Oy	5361	ttcagagctctgtggcccgagatgtccagagctgtccagctgtgacgtctctgtgcccctgtgtgtg	5420			
Dd	61	ttccaccttttggggcccttcgaatatcccaactgtccacagctgcgtcttcttgccctccctccgtgtggc	120			
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Db	121	GATGTGGGGGCCAGGACAGCTCAGCTCAGAGAGGCCAATTGACCAGATGTGCCGATGCCAG	180			
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Db	181	TATACCTTTCAGTGTGGCCAGTGTCCCAATGAATTCACACTGTCCAGACAGACAGCCAGGCATG	240			
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Db	241	TCAGTCAATCCAAATTAATTACAGAGACAGACAGCACCCCAACCGTTTAGACTGTGAGGCCACCC	300			
Qy	5601	aaagctgcagctcagctccctctgagagagctccctcccaacaaatgaaacttgaccctgacagctgac	5660			
Db	301	AAAGCTTCAGACTAGCTCCTCCTTGAGAGGCTCCTCCACCAATTGACTTGTGACCAAGCTGCC	360			
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Db	361	AGGCCCCAGAGAACCCAGAGAGGGGCTGCAGAGAGGAGTGGGCAACCTTGAGGGGGAGCGG	420			
Qy	5721	gaccgcctcggaaaccccaacacagagaagcttgagagactgctcagaaactcctccgagac	5780			
Db	421	GACCACTGTGAAACCCCAACCGAAGATTGGAGACTGTCTACAGCAACCTCTCTCCGAAC	480			
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ACCESSION	AR069089					
VERSION	AR069089.1	GI:6001296				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1999)					
AUTHORS	Nguyen,T.D., Polansky,J.R. and Huang,W.					
TITLE	Methods for the diagnosis of glaucoma.					
JOURNAL	Patent: US 5854415-A 2 29-DEC-1998;					
FEATURES	Location/Qualifiers					
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Db	61	TCGACGTTTGGGCGCTGAGATGTCCAGACTGTGCGAGCTGTCTTGCGCCGTGCGTGTGG	120			
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Db	121	GATGTGGGGGCCAGGACAGCTTACGTTCAAGGAAGGCCAATGACCAAGTGTGCCGATGCCAG	180			

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RESULT 13  
LOCUS HS085257 2000 bp mRNA PRI 19-MAR-1998  
DEFINITION Human trabecular meshwork Inducible glucocorticoid response protein  
(TIGR) mRNA, complete cds.  
ACCESSION U85257  
VERSION U85257.1 GI:2978428  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Nguyen,T.D. and Polansky,J.R.  
TITLE Glucocorticoid effects on HTM cells: Molecular Biology Approaches  
JOURNAL Glaucoma Update 4, 331-343 (1991)  
REFERENCE  
AUTHORS Stone,E.M., Fingert,J.H., Alward,W.L.M., Nguyen,T.D.,  
Nichols,B.E., Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and  
Sheffield,V.C.  
TITLE Identification of a gene that causes primary open angle glaucoma  
JOURNAL Science 275 (5300), 668-670 (1997)  
REFERENCE  
AUTHORS Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and  
Polansky,J.R.  
TITLE Gene structure and properties of TIGR, an olfactomedin-related  
glycoprotein cloned from glucocorticoid-induced trabecular meshwork  
cells  
JOURNAL J. Biol. Chem. 273 (11), 6341-6350 (1998)  
REFERENCE  
AUTHORS Nguyen,T.D. and Polansky,J.R.  
TITLE Direct Submission  
JOURNAL Submitted (13-JAN-1997) Ophthalmology, University of California San  
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA  
REFERENCE  
AUTHORS Nguyen,T.D.  
TITLE Direct Submission

JOURNAL Submitted (02-APR-1997) Ophthalmology, University of California San  
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA  
REMARK Sequence update by submitter  
REFERENCE 6 (bases 1 to 2000)  
AUTHORS Nguyen,T.D.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAR-1998) Ophthalmology, University of California San  
Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA  
REMARK Sequence update by submitter  
COMMENT On Mar 19, 1998 this sequence version replaced gi:1945067.  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 TCCAGCTTTGGGCGCGAGATGCGACCTGTCCAGCTGCTGCTTGTGCTGCTGCTG 120  
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Db 121 GATGTGGGGGCGCAGGAGCTCAGCTCAGGAGGCAATGACCAAGAGGCGGATGCCAG 180  
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RESULT 14  
AB4847  
LOCUS AB4847 2002 bp DNA PAT 21-JAN-2000  
DEFINITION Sequence 2 from Patent WO9844108.  
ACCESSION AB4847  
VERSION AB4847.1 GI:6733711  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2002)  
AUTHORS Huang, W. and Nguyen, T.D.  
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA  
JOURNAL Patent: WO 9844108-A 2 08-OCT-1998;  
HUANG WEIDONG (US); NGUYEN THAI D (US)  
FEATURES  
source Location/Qualifiers  
1. 2002  
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BASE COUNT 538 a 508 c 535 g 421 t  
ORIGIN

Query Match 10.4%; Score 640; DB 9; Length 2002;  
Best Local Similarity 100.0%; Pred. No. 0;  
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SOURCE human.  
ORGANISM human.

REFERENCE 1 (bases 1 to 2061)  
AUTHORS Escribano, J., Ortego, J., and Coca-Prados, M.  
TITLE Isolation and characterization of cell-specific cDNA clones from a  
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human donor: transcription and synthesis of plasma proteins  
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Polansky, J.R., Sundén, S.L.F., Nishimura, D., Clark, A.F., Nystuen, A.,  
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REFERENCE 3 (bases 1 to 2061)  
AUTHORS Ortego, J., Escribano, J., and Coca-Prados, M.  
TITLE Cloning and characterization of subtracted cDNAs from a human  
ciliary body library encoding TIGR, a protein involved in juvenile  
open angle glaucoma with homology to myosin and olfactomedin  
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JOURNAL MEDLINE 97424389

REFERENCE 4 (bases 1 to 2061)  
AUTHORS Coca-Prados, M., Ortego, J., and Escribano, J.  
TITLE Direct Submission  
JOURNAL Submitted (29-APR-1997) Ophthalmology and Visual Science, Yale  
University School Medicine, 330 Cedar St, New Haven, CT 06520, USA

FEATURES  
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1. 2061  
/gene="TIGR"  
/note="putative gene for Juvenile open angle glaucoma"  
23. 1537

gene  
CDS

